SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: Soderlund, David M.
                  Knipple, Douglas C.
                  Ingles, Patricia J.

    (ii) TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM
        INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT
        HOUSE FLIES

    (iii) NUMBER OF SEQUENCES: 19

    (iv) CORRESPONDENCE ADDRESS:
        (A) ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
        (B) STREET: P.O. Box 1051, Clinton Square
        (C) CITY: Rochester
        (D) STATE: New York
        (E) COUNTRY: USA
        (F) ZIP: 14603

    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER:
        (B) FILING DATE:
        (C) CLASSIFICATION:

    (vii) PRIOR APPLICATION DATA:
        (A) APPLICATION NUMBER: US 08/608,618
        (B) FILING DATE: 01-MAR-1996

    (viii) ATTORNEY/AGENT INFORMATION:
        (A) NAME: Braman, Susan J.
        (B) REGISTRATION NUMBER: 34,103
        (C) REFERENCE/DOCKET NUMBER: 19603/601 (CRF D-1657)

    (ix) TELECOMMUNICATION INFORMATION:
        (A) TELEPHONE: 716-263-1636
        (B) TELEFAX: 716-263-1600

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:

(A)  LENGTH: 6318 base pairs
(B)  TYPE: nucleic acid
(C)  STRANDEDNESS: single
(D)  TOPOLOGY: linear

(ii)  MOLECULE TYPE: cDNA


(xi)  SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
ATGACAGAAG ATTCCGACTC GATATCTGAG GAAGAACGCA GTTTGTTCCG TCCCTTCACC      60

CGCGAATCAT TGTTACAAAT CGAACAACGT ATCGCTGAAC ATGAAAAACA AAAGGAGCTG     120

GAAAGAAAGA GAGCCGCCGA AGGAGAGCAG ATACGATATG ATGACGAGGA CGAAGATGAA     180

GGTCCACAGC CGGATCCCAC ACTTGAACAG GGTGTGCCTA TACCTGTTCG AATGCAGGGC     240

AGCTTCCCGC CGGAATTGGC CTCCACTCCT CTCGAGGATA TCGATCCCTT CTACAGTAAT     300

GTACTGACAT TTGTAGTAAT AAGTAAAGGA AAGGATATTT TTCGTTTTTC TGCCTCAAAA     360

GCAATGTGGC TGCTCGATCC ATTCAATCCG ATACGTCGTG TAGCCATTTA TATTTTAGTG     420

CATCCCTTGT TTTCGTTATT CATTATCACC ACTATTCTAA CTAATTGTAT TTTAATGATA     480

ATGCCGACAA CGCCCACGGT CGAATCCACA GAGGTGATAT TCACCGGAAT CTACACATTT     540

GAATCAGCTG TTAAAGTGAT GGCACGAGGT TTCATTTTAT GCCCGTTTAC GTATCTTAGA     600

GATGCATGGA ATTGGCTGGA CTTCGTAGTA ATAGCTTTAG CTTATGTGAC CATGGGCATA     660

GATTTAGGTA ATCTCGCAGC TTTGAGAACA TTTAGGGTAC TGCGAGCTCT GAAAACCGTA     720

GCCATTGTGC CAGGTCTAAA AACCATTGTC GGTGCTGTCA TTGAATCTGT AAAAAATCTA     780

CGCGATGTGA TAATTTTGAC AATGTTTTCC CTGTCGGTGT CGCGCTGAT GGGCCTACAA      840

ATCTATATGG GTGTTCTAAC ACAAAGTGC ATTAAACGAT TCCCCCTGGA CGGCAGTTGG       900

GGCAATCTGA CCGATGAAAA CTGGTTTCTA CACAATAGCA ACAGTTCCAA TTGGTTTACG     960

GAGAACGATG GCGAGTCATA TCCGGTGTGC GGGAATGTAT CCGGTGCGGG ACAATGCGGC    1020

GAGGATTACG TCTGCCTGCA GGGCTTCGGC CCCAATCCCA ACTACGACTA CACCAGTTTC    1080

GATTCATTCG GTTGGGCTTT CCTGTCGGCG TTTCGTCTCA TGACCCAAGA TTTCTGGGAG    1140

GATCTGTATC AGCACGTGCT GCAAGCAGCT GGACCCTGGC ACATGTTGTT CTTTATAGTC    1200
```

```
ATCATCTTCC TAGGTTCATT CTATCTTGTG AATTTGATTT TGGCCATTGT TGCCATGTCT    1260

TATGACGAAT TGCAAAAGAA GGCCGAAGAA GAAGAGGCTG CCGAGGAGGA GGCGATACGA    1320

GAAGCTGAAG AAGCGGCAGC AGCCAAGGCG GCCAAACTGG AGGAGCGGGC CAATGTAGCA    1380

GCTCAAGCGG CTCAGGATGC AGCGGATGCC GCTGCGGCAG CTCTGCATCC CGAGATGGCA    1440

AAGAGTCCCA CGTACTCTTG CATTAGCTAT GAACTGTTTG TTGGCGGCGA GAAGGGCAAC    1500

GATGACAACA ACAAAGAGAA GATGTCCATA CGCAGCGTCG AAGTGGAATC GGAGTCGGTG    1560

AGCGTTATAC AAAGACAACC AGCACCTACC ACAGCACCCG CTACTAAAGT CCGTAAAGTT    1620

AGCACGACTT CCTTATCCTT ACCTGGTTCA CCATTTAACC TACGCCGGGG ATCACGTAGT    1680

TCACACAAGT ACACAATACG AAATGGGCGT GGACGTTTTG GTATACCAGG TAGCGATCGC    1740

AAGCCATTGG TACTGCAAAC ATATCAGGAT GCCCAGCAGC ATTTGCCCTA TGCCGATGAC    1800

TCGAATGCCG TAACACCAAT GTCCGAAGAG AATGGTGCCA TTATAGTACC AGCCTACTAT    1860

TGTAATTTAG GTTCTAGACA TTCTTCATAT ACCTCGCATC AATCAAGAAT CTCGTATACA    1920

TCACATGGTG ATTTATTGGG TGGCATGGCG GCCATGGGTG CCAGCACAAT GACCAAAGAG    1980

AGCAAATTGC GCAGTCGCAA CACACGCAAT CAATCAATCG GTGCTGCAAC CAATGGTGGC    2040

AGTAGTACGG CTGGTGGTGG CTATCCCGAT GCCAATCACA AGGAACAAAG GGATTATGAA    2100

ATGGGTCAGG ATTATACAGA CGAAGCTGGC AAAATAAAAC ACCACGACAA TCCTTTTATC    2160

GAGCCCGTCC AAACTCAAAC AGTGGTAGAC ATGAAAGATG TTATGGTCTT AAATGATATC    2220

ATTGAACAAG CCGCTGGTCG GCATAGTCGT GCTAGTGAAC GAGGTGAGGA CGATGACGAA    2280

GATGGTCCCA CATTCAAGGA CATCGCCCTC GAATACATCC TAAAAGGCAT CGAAATCTTT    2340

TGTGTATGGG ACTGTTGTTG GGTGTGGTTA AAATTTCAGG AATGGGTGTC CTTTATTGTG    2400

TTCGATCCAT TCGTGGAGCT CTTCATTACC CTGTGTATTG TGGTCAATAC GATGTTTATG    2460

GCCATGGATC ATCACGACAT GAATCCGGAA TTAGAGAAGG TGCTGAAAAG TGGTAACTAT    2520

TTCTTCACGG CCACTTTTGC AATTGAAGCC AGCATGAAAC TGATGGCCAT GAGCCCGAAG    2580

TACTACTTCC AGGAAGGCTG GAACATTTTC GATTTCATTA TTGTGGCCTT GTCTCTGCTG    2640
```

```
GAATTGGGCC TGGAGGGTGT CCAGGGCCTG TCGGTGTTGA GAAGTTTTCG TTTGCTTCGT      2700

GTATTCAAAT TGGCAAAATC ATGGCCCACA CTCAATTTAC TCATTTCGAT TATGGGCCGG      2760

ACAATGGGTG CATTGGGTAA TCTGACATTT GTACTTTGCA TTATCATCTT CATCTTTGCC      2820

GTGATGGGAA TGCAACTTTT CGGAAAGAAC TATATTGACC ACAAGGATCG CTTCAAGGAC      2880

CATGAATTAC CGCGCTGGAA CTTCACCGAC TTCATGCACA GCTTCATGAT TGTGTTCCGA      2940

GTGCTGTGCG GAGAGTGGAT CGAGTCCATG TGGGACTGCA TGTATGTGGG CGATGTCAGC      3000

TGTATACCCT TCTTCTTGGC CACGGTCGTG ATAGGCAATC TTGTGGTTCT TAATCTTTTC      3060

TTAGCTTTGC TTTTGTCCAA CTTCGGTTCA TCTAGTTTAT CAGCCCCGAC TGCCGACAAT      3120

GATACCAATA AAATAGCAGA GGCCTTCAAT CGTATTGCTC GTTTTAAGAA CTGGGTGAAA      3180

CGTAATATTG CCGATTGTTT TAAGTTAATT CGAAATAAAT TGACAAATCA AATAAGTGAC      3240

CAACCATCAG AACATGGCGA TAATGAACTG GAGTTGGGTC ATGACGAAAT CATGGGCGAT      3300

GGCTTGATCA AAAAGGGTAT GAAGGGCGAG ACCCAGCTGG AGGTGGCCAT TGGCGATGGC      3360

ATGGAGTTCA CGATACATGG CGATATGAAA AACAACAAGC CGAAGAAATC AAAATTCATG      3420

AACAACACAA CGATGATTGG AAACTCAATA AACCACCAAG ACAATAGACT GGAACATGAG      3480

CTAAACCATA GAGGTTTGTC CATACAGGAC GATGACACTG CCAGCATTAA CTCATATGGT      3540

AGCCATAAGA ATCGACCATT CAAGGACGAG AGCCACAAGG GCAGCGCCGA GACCATCGAG      3600

GGCGAGGAGA AACGCGACGT CAGCAAAGAG GACCTCGGCC TCGACGAGGA ACTGGACGAG      3660

GAGGCCGAGG GCGATGAGGG CCAGCTGGAT GGTGACATTA TCATTCATGC GCAAAACGAC      3720

GACGAGATAA TCGACGACTA TCCGGCCGAC TGTTTCCCCG ACTCGTACTA CAAGAAGTTT      3780

CCGATCTTGG CCGGCGACGA GGACTCGCCG TTCTGGCAAG GATGGGGCAA TTTACGACTG      3840

AAAACTTTTC AATTAATTGA AAATAAATAT TTTGAAACCG CAGTTATCAC TATGATTTTA      3900

ATGAGTAGCT TAGCTTTGGC CTTAGAAGAT GTTCATTTAC CCGATCGACC TGTCATGCAG      3960

GATATACTGT ACTACATGGA CAGGATATTT ACGGTGATAT TCTTTTTGGA GATGTTGATC      4020

AAATGGTTGG CCCTGGGCTT TAAGGTTTAC TTCACCAATG CCTGGTGTTG GCTGGATTTC      4080
```

```
GTGATTGTCA TGCTATCGCT TATAAATTTG GTTGCCGTTT GGTCGGGCTT AAATGATATA    4140

GCCGTGTTTA GATCAATGCG CACACTGCGC GCCCTAAGGC CATTGCGTGC TGTCTCTAGA    4200

TGGGAGGGTA TGAAAGTTGT CGTGAATGCG CTGGTTCAAG CTATACCGTC CATCTTCAAT    4260

GTGCTATTGG TGTGTCTGAT ATTTTGGCTT ATTTTTGCCA TTATGGGAGT ACAGCTTTTT    4320

GCTGGAAAAT ATTTTAAGTG TAAAGATGGT AATGACACTG TGCTGAGCCA TGAAATCATA    4380

CCGAATCGTA ATGCCTGCAA AAGTGAAAAC TACACCTGGG AAAATTCGGC AATGAACTTC    4440

GATCATGTAG GTAATGCGTA TCTCTGTCTA TTTCAAGTGG CCACCTTTAA GGGCTGGATC    4500

CAGATTATGA ACGATGCCAT TGATTCACGA GAGGTGGACA AGCAGCCGAT CCGAGAAACC    4560

AATATCTACA TGTATTTATA TTTCGTATTC TTCATTATAT TTGGATCATT TTTCACACTC    4620

AATCTGTTCA TTGGTGTTAT CATTGATAAT TTTAATGAAC AAAAGAAGAA AGCTGGTGGA    4680

TCATTAGAAA TGTTCATGAC AGAAGATCAG AAAAAGTACT ATAATGCTAT GAAAAAGATG    4740

GGCTCTAAAA AACCATTAAA AGCCATTCCA AGACCGAGGT GGCGACCACA AGCAATAGTA    4800

TTCGAAATAG TTACAGATAA AAAATTCGAT ATAATCATTA TGTTGTTCAT TGGCTTAAAC    4860

ATGTTTACCA TGACCCTCGA TCGGTACGAC GCCTCCGAGG CGTACAACAA TGTCCTCGAC    4920

AAACTCAATG GGATATTCGT AGTTATTTTC AGTGGCGAAT GTCTATTAAA AATATTCGCT    4980

TTACGATATC ACTATTTCAA AGAGCCATGG AATTTATTTG ATGTAGTAGT TGTCATTTTA    5040

TCCATCTTAG GTCTTGTACT CAGCGACATC ATTGAGAAGT ATTTCGTATC GCCGACACTG    5100

CTCCGTGTGG TGAGAGTGGC CAAAGTGGGT CGTGTCCTGC GTTTAGTCAA GGGTGCCAAG    5160

GGTATCCGGA CGTTGCTGTT CGCGTTAGCC ATGTCGTTGC CTGCCTTATT CAACATTTGT    5220

CTGTTGCTGT TCTTGGTGAT GTTCATCTTT GCTATCTTTG GCATGTCCTT CTTCATGCAT    5280

GTCAAAGAGA GAGCGGCAT AAATGCTGTG TATAATTTTA AGACATTTGG CCAAAGTATG    5340

ATATTGCTGT TTCAGATGTC TACCTCAGCC GGTTGGGATG GTGTGTTAGA TGCCATTATC    5400

AATGAGGAAG ATTGCGATCC ACCCGACAAC GACAAGGGCT ATCCGGGCAA TTGTGGTTCA    5460

GCGACTGTTG GAATTACGTT TCTCCTTTCA TATCTAGTTA TAAGCTTTTT GATAGTTATT    5520
```

```
AATATGTACA TTGCTGTCAT TCTCGAGAAC TATAGCCAGG CTACGGAGGA TGTACAGGAG        5580

GGTCTCACCG ACGACGATTA CGATATGTAC TACGAGATTT GGCAACAATT CGATCCGGAG        5640

GGCACCCAGT ACATACGCTA CGACCAGCTG TCCGAGTTTC TGGACGTGCT GGAGCCGCCG        5700

CTGCAGATCC ACAAGCCGAA CAAGTACAAA ATCATATCGA TGGACATGCC GATATGTCGG        5760

GGCGACATGA TGTACTGTGT GGATATATTG GATGCCCTGA CCAAGGACTT CTTTGCGCGC        5820

AAGGGTAATC CGATCGAGGA GACGGGTGAA ATTGGTGAGA TAGCGGCGCG ACCGGACACC        5880

GAGGGCTATG ATCCGGTGTC GTCAACACTG TGGCGCCAGC GTGAGGAGTA CTGCGCCAAG        5940

CTGATACAGA ATGCGTGGCG GCGTTACAAG AATGGCCCAC CCCAGGAGGG TGATGAGGGC        6000

GAGGCGGCTG GTGGCGAAGA TGGTGCTGAA GGCGGTGAGG GTGAAGGAGG CAGCGGCGGC        6060

GGCGGCGGTG ATGATGGTGG CTCAGCGACA GGAGCAACGG CGGCGGCGGG AGCCACATCA        6120

CCCTCAGATC CAGATGCCGG CGAAGCAGAT GGTGCCAGCG TCGGCGGCCC CCTTAGTCCG        6180

GGCTGTGTTA GTGGCGGCAG TAATGGCCGC CAAACGGCCG TACTGGTCGA AAGCGATGGT        6240

TTTGTTACAA AAAACGGTCA TAAGGTTGTA ATACACTCGA GATCGCCGAG CATAACATCC        6300

AGGACGGCAG ATGTCTGA                                                      6318
```

(2) INFORMATION FOR SEQ ID NO:2:

  (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 6315 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: cDNA

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
ATGACAGAAG ATTCCGACTC GATATCTGAG GAAGAACGCA GTTTGTTCCG TCCCTTCACC         60

CGCGAATCAT TGTTACAAAT CGAACAACGT ATCGCTGAAC ATGAAAAACA AAAGGAGCTG        120
```

```
GAAAGAAAGA GAGCCGCCGA AGGAGAGCAG ATACGATATG ATGACGAGGA CGAAGATGAA    180

GGTCCACAGC CGGATCCCAC ACTTGAACAG GGTGTGCCTA TACCTGTTCG AATGCAGGGC    240

AGCTTCCCGC CGGAATTGGC CTCCACTCCT CTCGAGGATA TCGATCCCTT CTACAGTAAT    300

GTACTGACAT TTGTAGTAAT AAGTAAAGGA AAGGATATTT TTCGTTTTTC TGCCTCAAAA    360

GCAATGTGGC TGCTCGATCC ATTCAATCCG ATACGTCGTG TAGCCATTTA TATTTTAGTG    420

CATCCCTTGT TTTCGTTATT CATTATCACC ACTATTCTAA CTAATTGTAT TTTAATGATA    480

ATGCCGACAA CGCCCACGGT CGAATCCACA GAGGTGATAT TCACCGGAAT CTACACATTT    540

GAATCAGCTG TTAAAGTGAT GGCACGAGGT TTCATTTTAT GCCCGTTTAC GTATCTTAGA    600

GATGCATGGA ATTGGCTGGA CTTCGTAGTA ATAGCTTTAG CTTATGTGAC CATGGGCATA    660

GATTTAGGTA ATCTCGCAGC TTTGAGAACA TTTAGGGTAC TGCGAGCTCT GAAAACCGTA    720

GCCATTGTGC CAGGTCTAAA AACCATTGTC GGTGCTGTCA TTGAATCTGT AAAAAATCTA    780

CGCGATGTGA TAATTTTGAC AATGTTTTCC CTGTCGGTGT TCGCGCTGAT GGGCCTACAA    840

ATCTATATGG GTGTTCTAAC ACAAAGTGC ATTAAACGAT TCCCCCTGGA CGGCAGTTGG    900

GGCAATCTGA CCGATGAAAA CTGGTTTCTA CACAATAGCA ACAGTTCCAA TTGGTTTACG    960

GAGAACGATG GCGAGTCATA TCCGGTGTGC GGGAATGTAT CCGGTGCGGG ACAATGCGGC    1020

GAAGATTACG TCTGCCTGCA GGGCTTCGGC CCCAATCCCA ACTACGACTA CACCAGTTTC    1080

GACTCATTCG GTTGGGCTTT CCTGTCGGCG TTTCGTCTCA TGACCCAAGA TTTCTGGGAG    1140

GATCTGTATC AGCACGTGCT GCAAGCAGCT GGACCCTGGC ACATGTTGTT CTTTATAGTC    1200

ATCATCTTCC TAGGTTCATT CTATCTTGTG AATTTGATTT TGGCCATTGT TGCCATGTCT    1260

TATGACGAAT TGCAAAAGAA GGCCGAAGAA GAAGAGGCTG CCGAGGAGGA GGCGATCCGA    1320

GAAGCTGAAG AAGCGGCAGC AGCCAAGGCG GCCAAACTGG AGGAGCGGGC CAATGTAGCA    1380

GCTCAAGCGG CTCAGGATGC AGCGGATGCC GCTGCGGCAG CTCTGCATCC CGAGATGGCA    1440

AAGAGTCCCA CGTACTCTTG CATTAGCTAT GAACTGTTTG TTGGCGGCGA GAAGGGCAAC    1500

GATGACAACA ACAAGGAGAA GATGTCGATA CGCAGCGTCG AAGTGGAATC GGAGTCGGTG    1560
```

```
AGCGTTATAC AAAGACAACC AGCACCTACC ACAGCACCCG CTACTAAAGT CCGTAAAGTT      1620

AGCACGACTT CCTTATCCTT ACCTGGTTCA CCATTTAACC TACGCCGGGG ATCACGTAGT      1680

TCACACAAGT ACACAATACG AAATGGGCGT GGACGTTTTG GTATACCAGG TAGCGATCGC      1740

AAGCCATTGG TACTGCAAAC ATATCAGGAT GCCCAGCAGC ATTTGCCCTA TGCCGATGAC      1800

TCGAATGCCG TAACACCAAT GTCCGAAGAG AATGGTGCCA TTATAGTACC AGCCTACTAT      1860

TGTAATTTAG GTTCTAGACA TTCTTCATAT ACCTCGCATC AATCAAGAAT CTCGTATACA      1920

TCACATGGTG ATTTATTGGG TGGCATGGCG GCCATGGGTG CCAGCACAAT GACCAAAGAG      1980

AGCAAATTGC GCAGTCGCAA CACACGCAAT CAATCAATCG GTGCTGCAAC CAATGGTGGC      2040

AGTAGTACGG CCGGTGGTGG CTATCCCGAT GCCAATCACA AGGAACAAAG GGATTATGAA      2100

AATGGGTCAGG ATTATACAGA CGAAGCTGGC AAAATAAAAC ACCACGACAA TCCTTTTATC     2160

GAGCCCGTCC AAACTCAAAC AGTGGTAGAC ATGAAAGATG TTATGGTCTT AAATGATATC     2220

ATTGAACAAG CCGCTGGTCG GCATAGTCGT GCTAGTGAAC GAGGTGAGGA CGATGACGAA      2280

GATGGTCCCA CATTCAAGGA CATCGCCCTC GAATATATCC TAAAAGGCAT CGAAATCTTT     2340

TGTGTATGGG ACTGTTGTTG GGTGTGGTTA AAATTTCAGG AATGGGTCTC CTTTATTGTG     2400

TTCGATCCAT TCGTGGAGCT CTTCATTACC CTGTGTATTG TGGTCAATAC AATGTTCATG     2460

GCCATGGATC ATCACGACAT GAATCCGGAA TTGGAGAAGG TGCTGAAAAG TGGTAACTAT     2520

TTCTTCACGG CCACTTTTGC AATTGAGGCC AGCATGAAAC TGATGGCCAT GAGCCCGAAG     2580

TACTACTTCC AGGAAGGCTG GAACATTTTC GATTTCATTA TTGTGGCCTT GTCTCTGCTG      2640

GAATTGGGCC TGGAGGGTGT CCAGGGCCTG TCGGTGTTGA GAAGTTTTCG TTTGCTTCGT      2700

GTATTCAAAT TGGCAAAATC ATGGCCCACA CTGAATTTAC TCATTTCGAT TATGGGCCGG      2760

ACAATGGGTG CATTGGGTAA TCTGACATTT GTACTTTGCA TTATCATCTT CATCTTTGCC      2820

GTGATGGGAA TGCAACTTTT CGGAAAGAAC TATATTGACC ACAAGGATCG CTTCAAGGAC      2880

CATGAATTAC CGCGCTGGAA TTTCACCGAC TTCATGCACA GCTTCATGAT TGTGTTCCGA      2940

GTGCTGTGCG GAGAGTGGAT CGAGTCCATG TGGGACTGCA TGTATGTGGG CGATGTCAGC      3000
```

```
TGTATACCCT TCTTCTTGGC CACGGTCGTG ATCGGCAATT TTGTGGTTCT TAATCTTTTC    3060

TTAGCTTTGC TTTTGTCCAA CTTCGGTTCA TCTAGTTTAT CAGCCCCGAC TGCCGACAAT    3120

GATACCAATA AAATAGCAGA GGCCTTCAAT CGTATTGCTC GTTTTAAGAA CTGGGTGAAA    3180

CGTAATATTG CCGATTGTTT TAAGTTAATT CGAAATAAAT TGACAAATCA AATAAGTGAC    3240

CAACCATCAG AACATGGCGA TAATGAACTG GAGTTGGGTC ATGACGAAAT CATGGGCGAT    3300

GGCTTGATCA AAAAGGGTAT GAAGGGCGAG ACCCAGCTGG AGGTGGCCAT TGGCGATGGC    3360

ATGGAGTTCA CGATACATGG CGATATGAAA AACAACAAGC CCAAGAAATC AAAATTCATA    3420

AACAACACAA CGATGATTGG AAACTCAATA AACCACCAAG ACAATAGACT GGAACATGAG    3480

GCTAAACCATA GAGGTTTGTC CATACAGGAC GATGACACTG CCAGCATTAA CTCATATGGT    3540

AGCCATAAGA ATCGACCATT CAAGGACGAG AGCCACAAGG GCAGCGCCGA GACCATCGAG    3600

GGCGAGGAGA AACGCGACGT CAGCAAAGAG GACCTCGGCC TCGACGAGGA ACTGGACGAG    3660

GAGGCCGAGG GCGATGAGGG CCAGCTGGAT GGTGACATCA TCATTCATGC CCAAAACGAC    3720

GACGAGATAA TCGACGACTA TCCGGCCGAC TGTTTCCCCG ACTCGTACTA CAAGAAGTTT    3780

CCGATCTTGG CCGGCGACGA GGACTCGCCG TTCTGGCAAG GATGGGGCAA TTTACGACTG    3840

AAAACTTTTC AATTAATTGA AAATAAATAT TTTGAAACCG CAGTTATCAC TATGATTTTA    3900

ATGAGTAGCT TAGCTTTGGC CTTAGAAGAT GTTCATTTAC CCGATCGACC TGTCATGCAG    3960

GATATACTGT ACTACATGGA CAGGATATTT ACGGTGATAT TCTTTTTGGA GATGTTGATC    4020

AAATGGTTGG CCCTGGGCTT TAAGGTCTAC TTCACCAATG CCTGGTGTTG GCTGGATTTC    4080

GTGATTGTCA TGCTATCGCT TATAAATTTG GTTGCCGTTT GGTCGGGCTT AAATGATATA    4140

GCCGTGTTTA GATCAATGCG CACACTGCGC GCCCTAAGGC CATTGCGTGC TGTCTCTAGA    4200

TGGGAGGGTA TGAAAGTTGT CGTGAATGCG CTGGTTCAAG CTATACCGTC CATCTTCAAT    4260

GTGCTATTGG TGTGTCTGAT ATTTTGGCTT ATTTTTGCCA TTATGGGAGT ACAGCTTTTT    4320

GCTGGAAAAT ATTTTAAGTG TAAAGATGGT AATGACACTG TGCTGAGCCA TGAAATCATA    4380

CCGAATCGTA ATGCCTGCAA AAGTGAAAAC TACACCTGGG AAAATTCGGC AATGAACTTC    4440
```

```
GATCATGTAG GTAATGCGTA TCTCTGTCTA TTTCAAGTGG CCACCTTTAA GGGCTGGATC    4500

CAGATTATGA ACGATGCCAT TGATTCACGA GAGGTGGACA AGCAGCCGAT CCGAGAAACC    4560

AATATCTACA TGTATTTATA TTTCGTATTC TTCATTATAT TTGGATCATT TTTCACACTC    4620

AATCTGTTCA TTGGTGTTAT CATTGATAAT TTTAATGAAC AAAAGAAGAA AGCAGGTGGA    4680

TCATTAGAAA TGTTCATGAC AGAAGATCAG AAAAAGTACT ATAATGCTAT GAAAAAGATG    4740

GGCTCTAAAA AACCATTAAA AGCCATTCCA AGACCGAGGT GGCGACCACA AGCAATAGTA    4800

TTCGAAATAG TTACAGATAA AAAATTCGAT ATAATCATTA TGTTGTTCAT TGGCTTAAAC    4860

ATGTTTACCA TGACCCTCGA TCGGTACGAC GCCTCCGAGG CGTACAACAA TGTCCTCGAC    4920

AAACTCAATG GGATATTCGT AGTTATTTTC AGTGGCGAAT GTCTATTAAA AATATTCGCT    4980

TTACGATATC ACTATTTCAA AGAGCCATGG AATTTATTTG ATGTAGTAGT TGTCATTTTA    5040

TCCATCTTAG GTCTTGTACT CAGCGACATC ATTGAGAAGT ATTTCGTATC GCCGACACTG    5100

CTCCGTGTGG TGAGAGTGGC CAAAGTGGGT CGTGTCCTGC GTTAGTCAA GGGTGCCAAG    5160

GGTATCCGGA CGTTGCTGTT CGCGTTAGCC ATGTCGTTGC CTGCCTTATT CAACATTTGT    5220

CTGTTGCTGT TCTTGGTGAT GTTCATCTTT GCTATCTTTG GCATGTCCTT CTTCATGCAT    5280

GTCAAAGAGA AGAGCGGCAT AAATGCTGTG TATAATTTTA AGACATTTGG CCAAAGTATG    5340

GATATTGCTGT TTCAGATGTC TACCTCAGCC GGTTGGGATG GTGTGTTAGA TGCCATTATC    5400

AATGAGGAAG ATTGCGATCC ACCCGACAAC GACAAGGGCT ATCCGGGCAA TTGTGGTTCA    5460

GCGACTGTTG GAATTACGTT TCTCCTTTCA TATCTAGTTA TAAGCTTTTT GATAGTTATT    5520

AATATGTACA TTGCTGTCAT TCTCGAGAAC TATAGCCAGG CTACGGAGGA TGTACAGGAG    5580

GGTCTCACCG ACGACGACTA TGATATGTAC TACGAGATTT GGCAACAATT CGATCCGGAG    5640

GGTACCCAGT ACATAAGATA CGACCAGCTG TCCGAGTTCC TGGACGTGCT GGAGCCGCCG    5700

CTGCAGATCC ACAAGCCGAA CAAGTACAAA ATCATATCGA TGGACATGCC GATATGTCGG    5760

GGCGACATGA TGTACTGTGT GGATATATTG GATGCCCTGA CCAAGGACTT CTTTGCGCGC    5820

AAGGGTAATC CGATCGAGGA GACGGGTGAA ATTGGTGAGA TTGCGGCGCG ACCGGACACC    5880
```

```
GAGGGCTATG ATCCGGTGTC GTCGACACTG TGGCGCCAGC GTGAGGAGTA CTGCGCCAAG      5940

CTGATACAGA ATGCGTGGCG GCGTTACAAG AATGGCCCAC CCCAGGAGGG TGATGAGGGC      6000

GAGGCGGCTG GTGGCGAAGA TGGTGCTGAA GGCGGTGAGG GTGAAGGCGG CAGCGGCGGC      6060

GGCGGCGATG ATGATGGTGG CTCAGCGACG GCGGCGGGAG CCACATCACC CACAGATCCA      6120

GATGCCGGCG AAGCAGATGG TGCCAGCGCC GGCAATGGTG GCGGCCCCCT TAGTCCGGGC      6180

TGTGTTAGTG GCGGCAGTAA TGGCCGCCAA ACGGCCGTAC TGGTCGAAAG CGATGGTTTT      6240

GTTACAAAAA ACGGTCATAA GGTTGTAATA CACTCGAGAT CGCCGAGCAT AACATCCAGG      6300

ACGGCAGATG TCTGA                                                      6315
```

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2105 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: not relevant
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
Met Thr Glu Asp Ser Asp Ser Ile Ser Glu Glu Glu Arg Ser Leu Phe
1               5                   10                  15

Arg Pro Phe Thr Arg Glu Ser Leu Leu Gln Ile Glu Gln Arg Ile Ala
            20                  25                  30

Glu His Glu Lys Gln Lys Glu Leu Glu Arg Lys Arg Ala Ala Glu Gly
            35                  40                  45

Glu Gln Ile Arg Tyr Asp Asp Glu Asp Glu Asp Glu Gly Pro Gln Pro
        50                  55                  60

Asp Pro Thr Leu Glu Gln Gly Val Pro Ile Pro Val Arg Met Gln Gly
65                  70                  75                  80

Ser Phe Pro Pro Glu Leu Ala Ser Thr Pro Leu Glu Asp Ile Asp Pro
                85                  90                  95
```

Phe Tyr Ser Asn Val Leu Thr Phe Val Val Ile Ser Lys Gly Lys Asp
            100             105             110

Ile Phe Arg Phe Ser Ala Ser Lys Ala Met Trp Leu Leu Asp Pro Phe
        115             120             125

Asn Pro Ile Arg Arg Val Ala Ile Tyr Ile Leu Val His Pro Leu Phe
    130             135             140

Ser Leu Phe Ile Ile Thr Thr Ile Leu Thr Asn Cys Ile Leu Met Ile
145             150             155             160

Met Pro Thr Thr Pro Thr Val Glu Ser Thr Glu Val Ile Phe Thr Gly
            165             170             175

Ile Tyr Thr Phe Glu Ser Ala Val Lys Val Met Ala Arg Gly Phe Ile
            180             185             190

Leu Cys Pro Phe Thr Tyr Leu Arg Asp Ala Trp Asn Trp Leu Asp Phe
        195             200             205

Val Val Ile Ala Leu Ala Tyr Val Thr Met Gly Ile Asp Leu Gly Asn
    210             215             220

Leu Ala Ala Leu Arg Thr Phe Arg Val Leu Arg Ala Leu Lys Thr Val
225             230             235             240

Ala Ile Val Pro Gly Leu Lys Thr Ile Val Gly Ala Val Ile Glu Ser
            245             250             255

Val Lys Asn Leu Arg Asp Val Ile Ile Leu Thr Met Phe Ser Leu Ser
        260             265             270

Val Phe Ala Leu Met Gly Leu Gln Ile Tyr Met Gly Val Leu Thr Gln
        275             280             285

Lys Cys Ile Lys Arg Phe Pro Leu Asp Gly Ser Trp Gly Asn Leu Thr
    290             295             300

Asp Glu Asn Trp Phe Leu His Asn Ser Asn Ser Ser Asn Trp Phe Thr
305             310             315             320

Glu Asn Asp Gly Glu Ser Tyr Pro Val Cys Gly Asn Val Ser Gly Ala
            325             330             335

Gly Gln Cys Gly Glu Asp Tyr Val Cys Leu Gln Gly Phe Gly Pro Asn
        340             345             350

Pro Asn Tyr Asp Tyr Thr Ser Phe Asp Ser Phe Gly Trp Ala Phe Leu
    355                  360                365

Ser Ala Phe Arg Leu Met Thr Gln Asp Phe Trp Glu Asp Leu Tyr Gln
    370                  375                380

His Val Leu Gln Ala Ala Gly Pro Trp His Met Leu Phe Phe Ile Val
385                390              395              400

Ile Ile Phe Leu Gly Ser Phe Tyr Leu Val Asn Leu Ile Leu Ala Ile
            405              410              415

Val Ala Met Ser Tyr Asp Glu Leu Gln Lys Lys Ala Glu Glu Glu Glu
        420              425                430

Ala Ala Glu Glu Glu Ala Ile Arg Glu Ala Glu Glu Ala Ala Ala Ala
        435              440              445

Lys Ala Ala Lys Leu Glu Glu Arg Ala Asn Val Ala Ala Gln Ala Ala
    450                455              460

Gln Asp Ala Ala Asp Ala Ala Ala Ala Leu His Pro Glu Met Ala
465                470              475              480

Lys Ser Pro Thr Tyr Ser Cys Ile Ser Tyr Glu Leu Phe Val Gly Gly
            485              490              495

Glu Lys Gly Asn Asp Asp Asn Asn Lys Glu Lys Met Ser Ile Arg Ser
        500              505              510

Val Glu Val Glu Ser Glu Ser Val Ser Val Ile Gln Arg Gln Pro Ala
        515              520              525

Pro Thr Thr Ala Pro Ala Thr Lys Val Arg Lys Val Ser Thr Thr Ser
    530                535              540

Leu Ser Leu Pro Gly Ser Pro Phe Asn Leu Arg Arg Gly Ser Arg Ser
545                550              555              560

Ser His Lys Tyr Thr Ile Arg Asn Gly Arg Gly Arg Phe Gly Ile Pro
            565              570              575

Gly Ser Asp Arg Lys Pro Leu Val Leu Gln Thr Tyr Gln Asp Ala Gln
        580              585              590

Gln His Leu Pro Tyr Ala Asp Asp Ser Asn Ala Val Thr Pro Met Ser
        595              600              605

Glu Glu Asn Gly Ala Ile Ile Val Pro Ala Tyr Tyr Cys Asn Leu Gly
    610                    615                 620

Ser Arg His Ser Ser Tyr Thr Ser His Gln Ser Arg Ile Ser Tyr Thr
625               630              635              640

Ser His Gly Asp Leu Leu Gly Gly Met Ala Ala Met Gly Ala Ser Thr
             645               650             655

Met Thr Lys Glu Ser Lys Leu Arg Ser Arg Asn Thr Arg Asn Gln Ser
             660               665             670

Ile Gly Ala Ala Thr Asn Gly Gly Ser Ser Thr Ala Gly Gly Gly Tyr
       675               680             685

Pro Asp Ala Asn His Lys Glu Gln Arg Asp Tyr Glu Met Gly Gln Asp
    690               695             700

Tyr Thr Asp Glu Ala Gly Lys Ile Lys His His Asp Asn Pro Phe Ile
705              710          715            720

Glu Pro Val Gln Thr Gln Thr Val Val Asp Met Lys Asp Val Met Val
           725            730          735

Leu Asn Asp Ile Ile Glu Gln Ala Ala Gly Arg His Ser Arg Ala Ser
         740            745          750

Glu Arg Gly Glu Asp Asp Asp Glu Asp Gly Pro Thr Phe Lys Asp Ile
       755               760          765

Ala Leu Glu Tyr Ile Leu Lys Gly Ile Glu Ile Phe Cys Val Trp Asp
    770              775              780

Cys Cys Trp Val Trp Leu Lys Phe Gln Glu Trp Val Ser Phe Ile Val
785              790          795          800

Phe Asp Pro Phe Val Glu Leu Phe Ile Thr Leu Cys Ile Val Val Asn
          805           810          815

Thr Met Phe Met Ala Met Asp His His Asp Met Asn Pro Glu Leu Glu
          820          825          830

Lys Val Leu Lys Ser Gly Asn Tyr Phe Phe Thr Ala Thr Phe Ala Ile
       835             840          845

Glu Ala Ser Met Lys Leu Met Ala Met Ser Pro Lys Tyr Tyr Phe Gln
    850              855          860

Glu Gly Trp Asn Ile Phe Asp Phe Ile Ile Val Ala Leu Ser Leu Leu
865             870             875             880

Glu Leu Gly Leu Glu Gly Val Gln Gly Leu Ser Val Leu Arg Ser Phe
            885             890             895

Arg Leu Leu Arg Val Phe Lys Leu Ala Lys Ser Trp Pro Thr Leu Asn
            900             905             910

Leu Leu Ile Ser Ile Met Gly Arg Thr Met Gly Ala Leu Gly Asn Leu
            915             920             925

Thr Phe Val Leu Cys Ile Ile Ile Phe Ile Phe Ala Val Met Gly Met
930             935             940

Gln Leu Phe Gly Lys Asn Tyr Ile Asp His Lys Asp Arg Phe Lys Asp
945             950             955             960

His Glu Leu Pro Arg Trp Asn Phe Thr Asp Phe Met His Ser Phe Met
            965             970             975

Ile Val Phe Arg Val Leu Cys Gly Glu Trp Ile Glu Ser Met Trp Asp
            980             985             990

Cys Met Tyr Val Gly Asp Val Ser Cys Ile Pro Phe Phe Leu Ala Thr
            995             1000            1005

Val Val Ile Gly Asn Leu Val Val Leu Asn Leu Phe Leu Ala Leu Leu
            1010            1015            1020

Leu Ser Asn Phe Gly Ser Ser Ser Leu Ser Ala Pro Thr Ala Asp Asn
1025            1030            1035            1040

Asp Thr Asn Lys Ile Ala Glu Ala Phe Asn Arg Ile Ala Arg Phe Lys
            1045            1050            1055

Asn Trp Val Lys Arg Asn Ile Ala Asp Cys Phe Lys Leu Ile Arg Asn
            1060            1065            1070

Lys Leu Thr Asn Gln Ile Ser Asp Gln Pro Ser Glu His Gly Asp Asn
            1075            1080            1085

Glu Leu Glu Leu Gly His Asp Glu Ile Met Gly Asp Gly Leu Ile Lys
            1090            1095            1100

Lys Gly Met Lys Gly Glu Thr Gln Leu Glu Val Ala Ile Gly Asp Gly
1105            1110            1115            1120

Met Glu Phe Thr Ile His Gly Asp Met Lys Asn Asn Lys Pro Lys Lys
            1125               1130              1135

Ser Lys Phe Met Asn Asn Thr Thr Met Ile Gly Asn Ser Ile Asn His
            1140               1145              1150

Gln Asp Asn Arg Leu Glu His Glu Leu Asn His Arg Gly Leu Ser Ile
      1155               1160              1165

Gln Asp Asp Asp Thr Ala Ser Ile Asn Ser Tyr Gly Ser His Lys Asn
      1170               1175              1180

Arg Pro Phe Lys Asp Glu Ser His Lys Gly Ser Ala Glu Thr Ile Glu
1185              1190             1195              1200

Gly Glu Glu Lys Arg Asp Val Ser Lys Glu Asp Leu Gly Leu Asp Glu
            1205              1210              1215

Glu Leu Asp Glu Glu Ala Glu Gly Asp Glu Gly Gln Leu Asp Gly Asp
            1220              1225              1230

Ile Ile Ile His Ala Gln Asn Asp Asp Glu Ile Ile Asp Asp Tyr Pro
        1235              1240              1245

Ala Asp Cys Phe Pro Asp Ser Tyr Tyr Lys Lys Phe Pro Ile Leu Ala
      1250               1255              1260

Gly Asp Glu Asp Ser Pro Phe Trp Gln Gly Trp Gly Asn Leu Arg Leu
1265              1270             1275              1280

Lys Thr Phe Gln Leu Ile Glu Asn Lys Tyr Phe Glu Thr Ala Val Ile
            1285              1290              1295

Thr Met Ile Leu Met Ser Ser Leu Ala Leu Ala Leu Glu Asp Val His
            1300              1305              1310

Leu Pro Asp Arg Pro Val Met Gln Asp Ile Leu Tyr Tyr Met Asp Arg
         1315              1320              1325

Ile Phe Thr Val Ile Phe Phe Leu Glu Met Leu Ile Lys Trp Leu Ala
        1330              1335              1340

Leu Gly Phe Lys Val Tyr Phe Thr Asn Ala Trp Cys Trp Leu Asp Phe
1345              1350             1355              1360

Val Ile Val Met Leu Ser Leu Ile Asn Leu Val Ala Val Trp Ser Gly
            1365              1370              1375

Leu Asn Asp Ile Ala Val Phe Arg Ser Met Arg Thr Leu Arg Ala Leu
     1380                1385              1390

Arg Pro Leu Arg Ala Val Ser Arg Trp Glu Gly Met Lys Val Val Val
     1395                1400              1405

Asn Ala Leu Val Gln Ala Ile Pro Ser Ile Phe Asn Val Leu Leu Val
     1410                1415              1420

Cys Leu Ile Phe Trp Leu Ile Phe Ala Ile Met Gly Val Gln Leu Phe
1425              1430              1435              1440

Ala Gly Lys Tyr Phe Lys Cys Lys Asp Gly Asn Asp Thr Val Leu Ser
           1445             1450              1455

His Glu Ile Ile Pro Asn Arg Asn Ala Cys Lys Ser Glu Asn Tyr Thr
           1460             1465              1470

Trp Glu Asn Ser Ala Met Asn Phe Asp His Val Gly Asn Ala Tyr Leu
     1475                1480              1485

Cys Leu Phe Gln Val Ala Thr Phe Lys Gly Trp Ile Gln Ile Met Asn
     1490                1495              1500

Asp Ala Ile Asp Ser Arg Glu Val Asp Lys Gln Pro Ile Arg Glu Thr
1505              1510              1515              1520

Asn Ile Tyr Met Tyr Leu Tyr Phe Val Phe Phe Ile Ile Phe Gly Ser
           1525             1530              1535

Phe Phe Thr Leu Asn Leu Phe Ile Gly Val Ile Ile Asp Asn Phe Asn
           1540             1545              1550

Glu Gln Lys Lys Lys Ala Gly Gly Ser Leu Glu Met Phe Met Thr Glu
           1555             1560              1565

Asp Gln Lys Lys Tyr Tyr Asn Ala Met Lys Lys Met Gly Ser Lys Lys
     1570                1575              1580

Pro Leu Lys Ala Ile Pro Arg Pro Arg Trp Arg Pro Gln Ala Ile Val
1585              1590              1595              1600

Phe Glu Ile Val Thr Asp Lys Lys Phe Asp Ile Ile Ile Met Leu Phe
           1605             1610              1615

Ile Gly Leu Asn Met Phe Thr Met Thr Leu Asp Arg Tyr Asp Ala Ser
           1620             1625              1630

```
Glu Ala Tyr Asn Asn Val Leu Asp Lys Leu Asn Gly Ile Phe Val Val
        1635             1640             1645

Ile Phe Ser Gly Glu Cys Leu Leu Lys Ile Phe Ala Leu Arg Tyr His
        1650             1655             1660

Tyr Phe Lys Glu Pro Trp Asn Leu Phe Asp Val Val Val Val Ile Leu
1665             1670             1675             1680

Ser Ile Leu Gly Leu Val Leu Ser Asp Ile Ile Glu Lys Tyr Phe Val
            1685             1690             1695

Ser Pro Thr Leu Leu Arg Val Val Arg Val Ala Lys Val Gly Arg Val
            1700             1705             1710

Leu Arg Leu Val Lys Gly Ala Lys Gly Ile Arg Thr Leu Leu Phe Ala
            1715             1720             1725

Leu Ala Met Ser Leu Pro Ala Leu Phe Asn Ile Cys Leu Leu Leu Phe
        1730             1735             1740

Leu Val Met Phe Ile Phe Ala Ile Phe Gly Met Ser Phe Phe Met His
1745             1750             1755             1760

Val Lys Glu Lys Ser Gly Ile Asn Ala Val Tyr Asn Phe Lys Thr Phe
            1765             1770             1775

Gly Gln Ser Met Ile Leu Leu Phe Gln Met Ser Thr Ser Ala Gly Trp
            1780             1785             1790

Asp Gly Val Leu Asp Ala Ile Ile Asn Glu Glu Asp Cys Asp Pro Pro
            1795             1800             1805

Asp Asn Asp Lys Gly Tyr Pro Gly Asn Cys Gly Ser Ala Thr Val Gly
        1810             1815             1820

Ile Thr Phe Leu Leu Ser Tyr Leu Val Ile Ser Phe Leu Ile Val Ile
1825             1830             1835             1840

Asn Met Tyr Ile Ala Val Ile Leu Glu Asn Tyr Ser Gln Ala Thr Glu
            1845             1850             1855

Asp Val Gln Glu Gly Leu Thr Asp Asp Tyr Asp Met Tyr Tyr Glu
            1860             1865             1870

Ile Trp Gln Gln Phe Asp Pro Glu Gly Thr Gln Tyr Ile Arg Tyr Asp
        1875             1880             1885
```

```
Gln Leu Ser Glu Phe Leu Asp Val Leu Glu Pro Pro Leu Gln Ile His
        1890            1895            1900

Lys Pro Asn Lys Tyr Lys Ile Ile Ser Met Asp Met Pro Ile Cys Arg
1905            1910            1915                    1920

Gly Asp Met Met Tyr Cys Val Asp Ile Leu Asp Ala Leu Thr Lys Asp
            1925            1930            1935

Phe Phe Ala Arg Lys Gly Asn Pro Ile Glu Glu Thr Gly Glu Ile Gly
            1940            1945            1950

Glu Ile Ala Ala Arg Pro Asp Thr Glu Gly Tyr Asp Pro Val Ser Ser
            1955            1960            1965

Thr Leu Trp Arg Gln Arg Glu Glu Tyr Cys Ala Lys Leu Ile Gln Asn
        1970            1975            1980

Ala Trp Arg Arg Tyr Lys Asn Gly Pro Pro Gln Glu Gly Asp Glu Gly
1985            1990            1995                    2000

Glu Ala Ala Gly Gly Glu Asp Gly Ala Glu Gly Gly Glu Gly Glu Gly
            2005            2010            2015

Gly Ser Gly Gly Gly Gly Gly Asp Asp Gly Gly Ser Ala Thr Gly Ala
            2020            2025            2030

Thr Ala Ala Ala Gly Ala Thr Ser Pro Ser Asp Pro Asp Ala Gly Glu
            2035            2040            2045

Ala Asp Gly Ala Ser Val Gly Gly Pro Leu Ser Pro Gly Cys Val Ser
        2050            2055            2060

Gly Gly Ser Asn Gly Arg Gln Thr Ala Val Leu Val Glu Ser Asp Gly
2065            2070            2075                    2080

Phe Val Thr Lys Asn Gly His Lys Val Val Ile His Ser Arg Ser Pro
            2085            2090            2095

Ser Ile Thr Ser Arg Thr Ala Asp Val
            2100            2105
```

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2104 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Met Thr Glu Asp Ser Asp Ser Ile Ser Glu Glu Glu Arg Ser Leu Phe
1               5                   10                  15

Arg Pro Phe Thr Arg Glu Ser Leu Leu Gln Ile Glu Gln Arg Ile Ala
            20                  25                  30

Glu His Glu Lys Gln Lys Glu Leu Glu Arg Lys Arg Ala Ala Glu Gly
        35                  40                  45

Glu Gln Ile Arg Tyr Asp Asp Glu Asp Glu Asp Glu Gly Pro Gln Pro
    50                  55                  60

Asp Pro Thr Leu Glu Gln Gly Val Pro Ile Pro Val Arg Met Gln Gly
65                  70                  75                  80

Ser Phe Pro Pro Glu Leu Ala Ser Thr Pro Leu Glu Asp Ile Asp Pro
            85                  90                  95

Phe Tyr Ser Asn Val Leu Thr Phe Val Val Ile Ser Lys Gly Lys Asp
            100                 105                 110

Ile Phe Arg Phe Ser Ala Ser Lys Ala Met Trp Leu Leu Asp Pro Phe
        115                 120                 125

Asn Pro Ile Arg Arg Val Ala Ile Tyr Ile Leu Val His Pro Leu Phe
    130                 135                 140

Ser Leu Phe Ile Ile Thr Thr Ile Leu Thr Asn Cys Ile Leu Met Ile
145                 150                 155                 160

Met Pro Thr Thr Pro Thr Val Glu Ser Thr Glu Val Ile Phe Thr Gly
            165                 170                 175

Ile Tyr Thr Phe Glu Ser Ala Val Lys Val Met Ala Arg Gly Phe Ile
            180                 185                 190

Leu Cys Pro Phe Thr Tyr Leu Arg Asp Ala Trp Asn Trp Leu Asp Phe
        195                 200                 205
```

```
Val Val Ile Ala Leu Ala Tyr Val Thr Met Gly Ile Asp Leu Gly Asn
    210             215             220

Leu Ala Ala Leu Arg Thr Phe Arg Val Leu Arg Ala Leu Lys Thr Val
225             230             235             240

Ala Ile Val Pro Gly Leu Lys Thr Ile Val Gly Ala Val Ile Glu Ser
            245             250             255

Val Lys Asn Leu Arg Asp Val Ile Ile Leu Thr Met Phe Ser Leu Ser
            260             265             270

Val Phe Ala Leu Met Gly Leu Gln Ile Tyr Met Gly Val Leu Thr Gln
        275             280             285

Lys Cys Ile Lys Arg Phe Pro Leu Asp Gly Ser Trp Gly Asn Leu Thr
    290             295             300

Asp Glu Asn Trp Phe Leu His Asn Ser Asn Ser Ser Asn Trp Phe Thr
305             310             315             320

Glu Asn Asp Gly Glu Ser Tyr Pro Val Cys Gly Asn Val Ser Gly Ala
            325             330             335

Gly Gln Cys Gly Glu Asp Tyr Val Cys Leu Gln Gly Phe Gly Pro Asn
        340             345             350

Pro Asn Tyr Asp Tyr Thr Ser Phe Asp Ser Phe Gly Trp Ala Phe Leu
        355             360             365

Ser Ala Phe Arg Leu Met Thr Gln Asp Phe Trp Glu Asp Leu Tyr Gln
370             375             380

His Val Leu Gln Ala Ala Gly Pro Trp His Met Leu Phe Phe Ile Val
385             390             395             400

Ile Ile Phe Leu Gly Ser Phe Tyr Leu Val Asn Leu Ile Leu Ala Ile
            405             410             415

Val Ala Met Ser Tyr Asp Glu Leu Gln Lys Lys Ala Glu Glu Glu Glu
            420             425             430

Ala Ala Glu Glu Glu Ala Ile Arg Glu Ala Glu Glu Ala Ala Ala Ala
        435             440             445

Lys Ala Ala Lys Leu Glu Glu Arg Ala Asn Val Ala Ala Gln Ala Ala
    450             455             460
```

```
Gln Asp Ala Ala Asp Ala Ala Ala Ala Ala Leu His Pro Glu Met Ala
465         470             475                 480

Lys Ser Pro Thr Tyr Ser Cys Ile Ser Tyr Glu Leu Phe Val Gly Gly
            485             490                 495

Glu Lys Gly Asn Asp Asp Asn Asn Lys Glu Lys Met Ser Ile Arg Ser
            500             505             510

Val Glu Val Glu Ser Glu Ser Val Ser Val Ile Gln Arg Gln Pro Ala
        515             520             525

Pro Thr Thr Ala Pro Ala Thr Lys Val Arg Lys Val Ser Thr Thr Ser
    530             535             540

Leu Ser Leu Pro Gly Ser Pro Phe Asn Leu Arg Arg Gly Ser Arg Ser
545             550             555                 560

Ser His Lys Tyr Thr Ile Arg Asn Gly Arg Gly Arg Phe Gly Ile Pro
            565             570             575

Gly Ser Asp Arg Lys Pro Leu Val Leu Gln Thr Tyr Gln Asp Ala Gln
            580             585             590

Gln His Leu Pro Tyr Ala Asp Asp Ser Asn Ala Val Thr Pro Met Ser
            595             600             605

Glu Glu Asn Gly Ala Ile Ile Val Pro Ala Tyr Tyr Cys Asn Leu Gly
    610             615             620

Ser Arg His Ser Ser Tyr Thr Ser His Gln Ser Arg Ile Ser Tyr Thr
625             630             635                 640

Ser His Gly Asp Leu Leu Gly Gly Met Ala Ala Met Gly Ala Ser Thr
            645             650             655

Met Thr Lys Glu Ser Lys Leu Arg Ser Arg Asn Thr Arg Asn Gln Ser
            660             665             670

Ile Gly Ala Ala Thr Asn Gly Gly Ser Ser Thr Ala Gly Gly Gly Tyr
        675             680             685

Pro Asp Ala Asn His Lys Glu Gln Arg Asp Tyr Glu Met Gly Gln Asp
    690             695             700

Tyr Thr Asp Glu Ala Gly Lys Ile Lys His His Asp Asn Pro Phe Ile
705             710             715             720
```

Glu Pro Val Gln Thr Gln Thr Val Val Asp Met Lys Asp Val Met Val
           725                 730              735

Leu Asn Asp Ile Ile Glu Gln Ala Ala Gly Arg His Ser Arg Ala Ser
          740           745             750

Glu Arg Gly Glu Asp Asp Asp Glu Asp Gly Pro Thr Phe Lys Asp Ile
       755           760           765

Ala Leu Glu Tyr Ile Leu Lys Gly Ile Glu Ile Phe Cys Val Trp Asp
   770           775           780

Cys Cys Trp Val Trp Leu Lys Phe Gln Glu Trp Val Ser Phe Ile Val
785           790          795             800

Phe Asp Pro Phe Val Glu Leu Phe Ile Thr Leu Cys Ile Val Val Asn
         805           810           815

Thr Met Phe Met Ala Met Asp His His Asp Met Asn Pro Glu Leu Glu
       820           825          830

Lys Val Leu Lys Ser Gly Asn Tyr Phe Phe Thr Ala Thr Phe Ala Ile
       835          840          845

Glu Ala Ser Met Lys Leu Met Ala Met Ser Pro Lys Tyr Tyr Phe Gln
   850           855          860

Glu Gly Trp Asn Ile Phe Asp Phe Ile Ile Val Ala Leu Ser Leu Leu
865          870          875             880

Glu Leu Gly Leu Glu Gly Val Gln Gly Leu Ser Val Leu Arg Ser Phe
         885           890          895

Arg Leu Leu Arg Val Phe Lys Leu Ala Lys Ser Trp Pro Thr Leu Asn
       900           905          910

Leu Leu Ile Ser Ile Met Gly Arg Thr Met Gly Ala Leu Gly Asn Leu
       915          920          925

Thr Phe Val Leu Cys Ile Ile Ile Phe Ile Phe Ala Val Met Gly Met
       930          935          940

Gln Leu Phe Gly Lys Asn Tyr Ile Asp His Lys Asp Arg Phe Lys Asp
945          950          955             960

His Glu Leu Pro Arg Trp Asn Phe Thr Asp Phe Met His Ser Phe Met
       965          970          975

Ile Val Phe Arg Val Leu Cys Gly Glu Trp Ile Glu Ser Met Trp Asp
        980             985             990

Cys Met Tyr Val Gly Asp Val Ser Cys Ile Pro Phe Phe Leu Ala Thr
     995            1000           1005

Val Val Ile Gly Asn Phe Val Val Leu Asn Leu Phe Leu Ala Leu Leu
  1010            1015           1020

Leu Ser Asn Phe Gly Ser Ser Ser Leu Ser Ala Pro Thr Ala Asp Asn
1025            1030          1035          1040

Asp Thr Asn Lys Ile Ala Glu Ala Phe Asn Arg Ile Ala Arg Phe Lys
        1045          1050          1055

Asn Trp Val Lys Arg Asn Ile Ala Asp Cys Phe Lys Leu Ile Arg Asn
        1060          1065          1070

Lys Leu Thr Asn Gln Ile Ser Asp Gln Pro Ser Glu His Gly Asp Asn
        1075          1080          1085

Glu Leu Glu Leu Gly His Asp Glu Ile Met Gly Asp Gly Leu Ile Lys
    1090            1095          1100

Lys Gly Met Lys Gly Glu Thr Gln Leu Glu Val Ala Ile Gly Asp Gly
1105            1110          1115          1120

Met Glu Phe Thr Ile His Gly Asp Met Lys Asn Asn Lys Pro Lys Lys
        1125          1130          1135

Ser Lys Phe Ile Asn Asn Thr Thr Met Ile Gly Asn Ser Ile Asn His
        1140          1145          1150

Gln Asp Asn Arg Leu Glu His Glu Leu Asn His Arg Gly Leu Ser Ile
        1155          1160          1165

Gln Asp Asp Asp Thr Ala Ser Ile Asn Ser Tyr Gly Ser His Lys Asn
    1170            1175          1180

Arg Pro Phe Lys Asp Glu Ser His Lys Gly Ser Ala Glu Thr Ile Glu
1185            1190          1195          1200

Gly Glu Glu Lys Arg Asp Val Ser Lys Glu Asp Leu Gly Leu Asp Glu
        1205          1210          1215

Glu Leu Asp Glu Glu Ala Glu Gly Asp Glu Gly Gln Leu Asp Gly Asp
        1220          1225          1230

Ile Ile Ile His Ala Gln Asn Asp Asp Glu Ile Ile Asp Asp Tyr Pro
        1235           1240                1245

Ala Asp Cys Phe Pro Asp Ser Tyr Tyr Lys Lys Phe Pro Ile Leu Ala
    1250           1255             1260

Gly Asp Glu Asp Ser Pro Phe Trp Gln Gly Trp Gly Asn Leu Arg Leu
1265           1270           1275           1280

Lys Thr Phe Gln Leu Ile Glu Asn Lys Tyr Phe Glu Thr Ala Val Ile
        1285           1290           1295

Thr Met Ile Leu Met Ser Ser Leu Ala Leu Ala Leu Glu Asp Val His
      1300           1305           1310

Leu Pro Asp Arg Pro Val Met Gln Asp Ile Leu Tyr Tyr Met Asp Arg
      1315           1320           1325

Ile Phe Thr Val Ile Phe Phe Leu Glu Met Leu Ile Lys Trp Leu Ala
      1330           1335           1340

Leu Gly Phe Lys Val Tyr Phe Thr Asn Ala Trp Cys Trp Leu Asp Phe
1345           1350           1355           1360

Val Ile Val Met Leu Ser Leu Ile Asn Leu Val Ala Val Trp Ser Gly
        1365           1370           1375

Leu Asn Asp Ile Ala Val Phe Arg Ser Met Arg Thr Leu Arg Ala Leu
        1380           1385           1390

Arg Pro Leu Arg Ala Val Ser Arg Trp Glu Gly Met Lys Val Val Val
      1395           1400           1405

Asn Ala Leu Val Gln Ala Ile Pro Ser Ile Phe Asn Val Leu Leu Val
      1410           1415           1420

Cys Leu Ile Phe Trp Leu Ile Phe Ala Ile Met Gly Val Gln Leu Phe
1425           1430           1435           1440

Ala Gly Lys Tyr Phe Lys Cys Lys Asp Gly Asn Asp Thr Val Leu Ser
        1445           1450           1455

His Glu Ile Ile Pro Asn Arg Asn Ala Cys Lys Ser Glu Asn Tyr Thr
        1460           1465           1470

Trp Glu Asn Ser Ala Met Asn Phe Asp His Val Gly Asn Ala Tyr Leu
      1475           1480           1485

Cys Leu Phe Gln Val Ala Thr Phe Lys Gly Trp Ile Gln Ile Met Asn
   1490                1495                 1500

Asp Ala Ile Asp Ser Arg Glu Val Asp Lys Gln Pro Ile Arg Glu Thr
1505            1510            1515                 1520

Asn Ile Tyr Met Tyr Leu Tyr Phe Val Phe Phe Ile Ile Phe Gly Ser
         1525               1530               1535

Phe Phe Thr Leu Asn Leu Phe Ile Gly Val Ile Ile Asp Asn Phe Asn
        1540              1545            1550

Glu Gln Lys Lys Lys Ala Gly Gly Ser Leu Glu Met Phe Met Thr Glu
        1555             1560           1565

Asp Gln Lys Lys Tyr Tyr Asn Ala Met Lys Lys Met Gly Ser Lys Lys
    1570              1575            1580

Pro Leu Lys Ala Ile Pro Arg Pro Arg Trp Arg Pro Gln Ala Ile Val
1585              1590           1595              1600

Phe Glu Ile Val Thr Asp Lys Lys Phe Asp Ile Ile Ile Met Leu Phe
        1605              1610           1615

Ile Gly Leu Asn Met Phe Thr Met Thr Leu Asp Arg Tyr Asp Ala Ser
        1620             1625           1630

Glu Ala Tyr Asn Asn Val Leu Asp Lys Leu Asn Gly Ile Phe Val Val
        1635             1640           1645

Ile Phe Ser Gly Glu Cys Leu Leu Lys Ile Phe Ala Leu Arg Tyr His
        1650             1655           1660

Tyr Phe Lys Glu Pro Trp Asn Leu Phe Asp Val Val Val Val Ile Leu
1665              1670           1675              1680

Ser Ile Leu Gly Leu Val Leu Ser Asp Ile Ile Glu Lys Tyr Phe Val
        1685             1690           1695

Ser Pro Thr Leu Leu Arg Val Val Arg Val Ala Lys Val Gly Arg Val
        1700             1705           1710

Leu Arg Leu Val Lys Gly Ala Lys Gly Ile Arg Thr Leu Leu Phe Ala
        1715             1720           1725

Leu Ala Met Ser Leu Pro Ala Leu Phe Asn Ile Cys Leu Leu Leu Phe
        1730             1735           1740

Leu Val Met Phe Ile Phe Ala Ile Phe Gly Met Ser Phe Phe Met His
1745                1750              1755                      1760

Val Lys Glu Lys Ser Gly Ile Asn Ala Val Tyr Asn Phe Lys Thr Phe
            1765              1770                  1775

Gly Gln Ser Met Ile Leu Leu Phe Gln Met Ser Thr Ser Ala Gly Trp
            1780              1785                  1790

Asp Gly Val Leu Asp Ala Ile Ile Asn Glu Glu Asp Cys Asp Pro Pro
        1795              1800              1805

Asp Asn Asp Lys Gly Tyr Pro Gly Asn Cys Gly Ser Ala Thr Val Gly
    1810              1815              1820

Ile Thr Phe Leu Leu Ser Tyr Leu Val Ile Ser Phe Leu Ile Val Ile
1825              1830              1835                      1840

Asn Met Tyr Ile Ala Val Ile Leu Glu Asn Tyr Ser Gln Ala Thr Glu
            1845              1850                  1855

Asp Val Gln Glu Gly Leu Thr Asp Asp Asp Tyr Asp Met Tyr Tyr Glu
            1860              1865                  1870

Ile Trp Gln Gln Phe Asp Pro Glu Gly Thr Gln Tyr Ile Arg Tyr Asp
        1875              1880              1885

Gln Leu Ser Glu Phe Leu Asp Val Leu Glu Pro Pro Leu Gln Ile His
    1890              1895              1900

Lys Pro Asn Lys Tyr Lys Ile Ile Ser Met Asp Met Pro Ile Cys Arg
1905              1910              1915                      1920

Gly Asp Met Met Tyr Cys Val Asp Ile Leu Asp Ala Leu Thr Lys Asp
            1925              1930                  1935

Phe Phe Ala Arg Lys Gly Asn Pro Ile Glu Glu Thr Gly Glu Ile Gly
            1940              1945                  1950

Glu Ile Ala Ala Arg Pro Asp Thr Glu Gly Tyr Asp Pro Val Ser Ser
    1955              1960              1965

Thr Leu Trp Arg Gln Arg Glu Glu Tyr Cys Ala Lys Leu Ile Gln Asn
    1970              1975              1980

Ala Trp Arg Arg Tyr Lys Asn Gly Pro Pro Gln Glu Gly Asp Glu Gly
1985              1990              1995                      2000

```
Glu Ala Ala Gly Gly Glu Asp Gly Ala Glu Gly Gly Glu Gly Glu Gly
              2005                2010                2015

Gly Ser Gly Gly Gly Gly Asp Asp Asp Gly Gly Ser Ala Thr Ala Ala
              2020                2025                2030

Gly Ala Thr Ser Pro Thr Asp Pro Asp Ala Gly Glu Ala Asp Gly Ala
              2035                2040                2045

Ser Ala Gly Asn Gly Gly Gly Pro Leu Ser Pro Gly Cys Val Ser Gly
         2050                2055                2060

Gly Ser Asn Gly Arg Gln Thr Ala Val Leu Val Glu Ser Asp Gly Phe
2065                2070                2075                2080

Val Thr Lys Asn Gly His Lys Val Val Ile His Ser Arg Ser Pro Ser
              2085                2090                2095

Ile Thr Ser Arg Thr Ala Asp Val
              2100
```

(2)  INFORMATION FOR SEQ ID NO:5:

    (i)  SEQUENCE CHARACTERISTICS:
        (A)  LENGTH: 18 base pairs
        (B)  TYPE: nucleic acid
        (C)  STRANDEDNESS: single
        (D)  TOPOLOGY: linear

   (ii)  MOLECULE TYPE: cDNA


   (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGTTGGGCT TTCCTGTC                                                      18

(2)  INFORMATION FOR SEQ ID NO:6:

    (i)  SEQUENCE CHARACTERISTICS:
        (A)  LENGTH: 26 base pairs
        (B)  TYPE: nucleic acid
        (C)  STRANDEDNESS: single
        (D)  TOPOLOGY: linear

   (ii)  MOLECULE TYPE: cDNA


   (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGGAATTCRA ADATRTTCCA NCCYTC                                    26

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 23 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCCGARGAYA THGAYCYNTA YTA                                       23

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCGTATCGCCT CCTCCTCG                                            18

(2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 29 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGTCTAGAT HTTYGCNATH TTYGGNATG                                 29

(2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 27 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGGAATTCN GGRTCRAAYT GYTGCCA                 27

(2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 27 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGGTCTAGAR GANCARAARA ARTAYTA               27

(2) INFORMATION FOR SEQ ID NO:12:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 20 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TCATACTTTG GCCCAATGTC                     20

(2) INFORMATION FOR SEQ ID NO:13:

    (i) SEQUENCE CHARACTERISTICS:

       (A) LENGTH: 21 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: cDNA

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCCGAATTAG AGAAGGTGCT G                    21

(2) INFORMATION FOR SEQ ID NO:14:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 21 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: cDNA

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ACTATTGCTT GTGGTCGCCA C                    21

(2) INFORMATION FOR SEQ ID NO:15:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 25 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: cDNA

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CATCNTTRGC NGCNTAGACN ATGAC               25

(2) INFORMATION FOR SEQ ID NO:16:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 21 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single

            (D)  TOPOLOGY:  linear

     (ii)  MOLECULE TYPE:  cDNA


     (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:16:

GATTGAATGG ATCGAGCAGC C                                                    21

  (2)  INFORMATION FOR SEQ ID NO:17:

        (i)  SEQUENCE CHARACTERISTICS:
             (A)  LENGTH:  21 base pairs
             (B)  TYPE:  nucleic acid
             (C)  STRANDEDNESS:  single
             (D)  TOPOLOGY:  linear

        (ii)  MOLECULE TYPE:  cDNA


        (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:17:

CGTTTCTCCT TTCATATCTA G                                                    21

  (2)  INFORMATION FOR SEQ ID NO:18:

        (i)  SEQUENCE CHARACTERISTICS:
             (A)  LENGTH:  25 base pairs
             (B)  TYPE:  nucleic acid
             (C)  STRANDEDNESS:  single
             (D)  TOPOLOGY:  linear

        (ii)  MOLECULE TYPE:  cDNA


        (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:18:

GGAGBGGBGG NCKBGGNCKN GCTCA                                                25

  (2)  INFORMATION FOR SEQ ID NO:19:

        (i)  SEQUENCE CHARACTERISTICS:
             (A)  LENGTH:  2100 amino acids
             (B)  TYPE:  amino acid
             (C)  STRANDEDNESS:  not relevant
             (D)  TOPOLOGY:  linear

        (ii)  MOLECULE TYPE:  protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
Met Thr Glu Asp Ser Asp Ser Ile Ser Glu Glu Glu Arg Ser Leu Phe
1               5                   10                  15

Arg Pro Phe Thr Arg Glu Ser Leu Val Gln Ile Glu Gln Arg Ile Ala
                20                  25                  30

Ala Glu His Glu Lys Gln Lys Glu Leu Glu Arg Lys Arg Ala Glu Gly
            35                  40                  45

Glu Val Pro Arg Tyr Gly Arg Lys Lys Lys Gln Lys Glu Ile Arg Tyr
        50                  55                  60

Asp Asp Glu Asp Glu Asp Glu Gly Pro Gln Pro Asp Pro Thr Leu Glu
65                  70                  75                  80

Gln Gly Val Pro Ile Pro Val Arg Leu Gln Gly Ser Phe Pro Pro Glu
                85                  90                  95

Leu Ala Ser Thr Pro Leu Glu Asp Ile Asp Pro Tyr Tyr Ser Asn Val
            100                 105                 110

Leu Thr Phe Val Val Val Ser Lys Gly Lys Asp Ile Phe Arg Phe Ser
        115                 120                 125

Ala Ser Lys Ala Met Trp Met Leu Asp Pro Phe Asn Pro Ile Arg Arg
    130                 135                 140

Val Ala Ile Tyr Ile Leu Val His Pro Leu Phe Ser Leu Phe Ile Ile
145                 150                 155                 160

Thr Thr Ile Leu Val Asn Cys Ile Leu Met Ile Met Pro Thr Thr Pro
                165                 170                 175

Thr Val Glu Ser Thr Glu Val Ile Phe Thr Gly Ile Tyr Thr Phe Glu
                180                 185                 190

Ser Ala Val Lys Val Met Ala Arg Gly Phe Ile Leu Cys Pro Phe Thr
        195                 200                 205

Tyr Leu Arg Asp Ala Trp Asn Trp Leu Asp Phe Val Val Ile Ala Leu
    210                 215                 220

Ala Tyr Val Thr Met Gly Ile Asp Leu Gly Asn Leu Ala Ala Leu Arg
225                 230                 235                 240
```

Thr Phe Arg Val Leu Arg Ala Leu Lys Thr Val Ala Ile Val Pro Gly
                    245             250                 255

Leu Lys Thr Ile Val Gly Ala Val Ile Glu Ser Val Lys Asn Leu Arg
            260             265             270

Asp Val Ile Ile Leu Thr Met Phe Ser Leu Ser Val Phe Ala Leu Met
        275             280             285

Gly Leu Gln Ile Tyr Met Gly Val Leu Thr Glu Lys Cys Ile Lys Lys
    290             295             300

Phe Pro Leu Asp Gly Ser Trp Gly Asn Leu Thr Asp Glu Asn Trp Asp
305             310             315             320

Tyr His Asn Arg Asn Ser Ser Asn Trp Tyr Ser Glu Asp Glu Gly Ile
            325             330             335

Ser Phe Pro Leu Cys Gly Asn Ile Ser Gly Ala Gly Gln Cys Asp Asp
            340             345             350

Asp Tyr Val Cys Leu Gln Gly Phe Gly Pro Asn Pro Asn Tyr Gly Tyr
        355             360             365

Thr Ser Phe Asp Ser Phe Gly Trp Ala Phe Leu Ser Ala Phe Arg Leu
    370             375             380

Met Thr Gln Asp Phe Trp Glu Asp Leu Tyr Gln Leu Val Leu Arg Ala
385             390             395             400

Ala Gly Pro Trp His Met Leu Phe Phe Ile Val Ile Ile Phe Leu Gly
            405             410             415

Ser Phe Tyr Leu Val Asn Leu Ile Leu Ala Ile Val Ala Met Ser Tyr
            420             425             430

Asp Glu Leu Gln Arg Lys Ala Glu Glu Glu Ala Ala Glu Glu Glu
        435             440             445

Ala Ile Arg Glu Ala Glu Glu Ala Ala Ala Lys Ala Ala Lys Leu
    450             455             460

Glu Glu Arg Ala Asn Ala Gln Ala Gln Ala Ala Ala Asp Ala Ala Ala
465             470             475             480

Ala Glu Glu Ala Ala Leu His Pro Glu Met Ala Lys Ser Pro Thr Tyr

```
                485                        490                        495
Ser Cys Ile Ser Tyr Glu Leu Phe Val Gly Gly Glu Lys Gly Asn Asp
            500                      505                      510

Asp Asn Asn Lys Glu Lys Met Ser Ile Arg Ser Val Glu Val Glu Ser
            515                      520                      525

Glu Ser Val Ser Val Ile Gln Arg Gln Pro Ala Pro Thr Thr Ala His
            530                      535                      540

Gln Ala Thr Lys Val Arg Lys Val Ser Thr Thr Ser Leu Ser Leu Pro
545                      550                      555                      560

Gly Ser Pro Phe Asn Ile Arg Arg Gly Ser Arg Ser Ser His Lys Tyr
                565                      570                      575

Thr Ile Arg Asn Gly Arg Gly Arg Phe Gly Ile Pro Gly Ser Asp Arg
            580                      585                      590

Lys Pro Leu Val Leu Ser Thr Tyr Gln Asp Ala Gln Gln His Leu Pro
            595                      600                      605

Tyr Ala Asp Asp Ser Asn Ala Val Thr Pro Met Ser Glu Glu Asn Gly
            610                      615                      620

Ala Ile Ile Val Pro Val Tyr Tyr Gly Asn Leu Gly Ser Arg His Ser
625                      630                      635                      640

Ser Tyr Thr Ser His Gln Ser Arg Ile Ser Tyr Thr Ser His Gly Asp
                645                      650                      655

Leu Leu Gly Gly Met Ala Val Met Gly Val Ser Thr Met Thr Lys Glu
                660                      665                      670


Ser Lys Leu Arg Asn Arg Asn Thr Arg Asn Gln Ser Val Gly Ala Thr
            675                      680                      685

Asn Gly Gly Thr Thr Cys Leu Asp Thr Asn His Lys Leu Asp His Arg
    690                      695                      700

Asp Tyr Glu Ile Gly Leu Glu Cys Thr Asp Glu Ala Gly Lys Ile Lys
705                      710                      715                      720

His His Asp Asn Pro Phe Ile Glu Pro Val Gln Thr Gln Thr Val Val
                725                      730                      735
```

Asp Met Lys Asp Val Met Val Leu Asn Asp Ile Ile Glu Gln Ala Ala
            740             745             750

Gly Arg His Ser Arg Ala Ser Asp Arg Gly Glu Asp Asp Asp Glu Asp
            755             760             765

Gly Pro Thr Phe Lys Asp Lys Ala Leu Glu Val Ile Leu Lys Gly Ile
    770             775             780

Asp Val Phe Cys Val Trp Asp Cys Cys Trp Val Trp Leu Lys Phe Gln
785             790             795             800

Glu Trp Val Ser Leu Ile Val Phe Asp Pro Phe Val Glu Leu Phe Ile
            805             810             815

Thr Leu Cys Ile Val Val Asn Thr Met Phe Met Ala Met Asp His His
            820             825             830

Asp Met Asn Lys Glu Met Glu Arg Val Leu Lys Ser Gly Asn Tyr Phe
            835             840             845

Phe Thr Ala Thr Phe Ala Ile Glu Ala Thr Met Lys Leu Met Ala Met
    850             855             860

Ser Pro Lys Tyr Tyr Phe Gln Glu Gly Trp Asn Ile Phe Asp Phe Ile
865             870             875             880

Ile Val Ala Leu Ser Leu Leu Glu Leu Gly Leu Glu Gly Val Gln Gly
            885             890             895

Leu Ser Val Leu Arg Ser Phe Arg Leu Leu Arg Val Phe Lys Leu Ala
            900             905             910

Lys Ser Trp Pro Thr Leu Asn Leu Leu Ile Ser Ile Met Gly Arg Thr
            915             920             925

Met Gly Ala Leu Gly Asn Leu Thr Phe Val Leu Cys Ile Ile Ile Phe
    930             935             940

Ile Phe Ala Val Met Gly Met Gln Leu Phe Gly Lys Asn Tyr His Asp
945             950             955             960

His Lys Asp Arg Phe Pro Asp Gly Asp Leu Pro Arg Trp Asn Phe Thr
            965             970             975

Asp Phe Met His Ser Phe Met Ile Val Phe Arg Val Leu Cys Gly Glu
            980             985             990

Trp Ile Glu Ser Met Trp Asp Cys Met Tyr Val Gly Asp Val Ser Cys
    995                    1000            1005

Ile Pro Phe Phe Leu Ala Thr Val Val Ile Gly Asn Leu Val Val Leu
    1010                  1015            1020

Asn Leu Phe Leu Ala Leu Leu Leu Ser Asn Phe Gly Ser Ser Ser Leu
1025              1030            1035            1040

Ser Ala Pro Thr Ala Asp Asn Asp Thr Asn Lys Ile Ala Glu Ala Phe
             1045            1050           1055

Asn Arg Ile Gly Arg Phe Lys Ser Trp Val Lys Arg Asn Ile Ala Asp
       1060              1065           1070

Cys Phe Lys Leu Ile Arg Asn Lys Leu Thr Asn Gln Ile Ser Asp Gln
      1075             1080           1085

Pro Ser Glu His Gly Asp Asn Glu Leu Glu Leu Gly His Asp Glu Ile
    1090              1095           1100

Leu Ala Asp Gly Leu Ile Lys Lys Gly Ile Lys Glu Gln Thr Gln Leu
1105           1110            1115           1120

Glu Val Ala Ile Gly Asp Gly Met Glu Phe Thr Ile His Gly Asp Met
         1125           1130           1135

Lys Asn Asn Lys Pro Lys Lys Ser Lys Tyr Leu Asn Asn Ala Thr Asp
       1140             1145           1150

Asp Asp Thr Ala Ser Ile Asn Ser Tyr Gly Ser His Lys Asn Arg Pro
      1155           1160           1165

Phe Lys Asp Glu Ser His Lys Gly Ser Ala Glu Thr Met Glu Gly Glu
    1170           1175           1180

Glu Lys Arg Asp Ala Ser Lys Glu Asp Leu Gly Leu Asp Glu Glu Leu
1185           1190           1195           1200

Asp Glu Glu Gly Glu Cys Glu Glu Gly Pro Leu Asp Gly Asp Ile Ile
         1205           1210           1215

Ile His Ala His Asp Glu Asp Ile Leu Asp Glu Tyr Pro Ala Asp Cys
      1220           1225           1230

Cys Pro Asp Ser Tyr Tyr Lys Lys Phe Pro Ile Leu Ala Gly Asp Asp
     1235            1240           1245

```
Asp Ser Pro Phe Trp Gln Gly Trp Gly Asn Leu Arg Leu Lys Thr Phe
    1250              1255              1260

Arg Leu Ile Glu Asp Lys Tyr Phe Glu Thr Ala Val Ile Thr Met Ile
1265              1270              1275              1280

Leu Met Ser Ser Leu Ala Leu Ala Leu Glu Asp Val His Leu Pro Gln
              1285              1290              1295

Arg Pro Ile Leu Gln Asp Ile Leu Tyr Tyr Met Asp Arg Ile Phe Thr
              1300              1305              1310

Val Ile Phe Phe Leu Glu Met Leu Ile Lys Trp Leu Ala Leu Gly Phe
              1315              1320              1325

Lys Val Tyr Leu Thr Asn Ala Trp Cys Trp Leu Asp Phe Val Ile Val
    1330              1335              1340

Met Val Ser Leu Ile Asn Phe Val Ala Ser Leu Val Gly Ala Gly Gly
1345              1350              1355              1360

Ile Gln Ala Phe Lys Thr Met Arg Thr Leu Arg Ala Leu Arg Pro Leu
              1365              1370              1375

Arg Ala Met Ser Arg Met Gln Gly Met Arg Val Val Val Asn Ala Leu
              1380              1385              1390

Val Gln Ala Ile Pro Ser Ile Phe Asn Val Leu Leu Val Cys Leu Ile
              1395              1400              1405

Phe Trp Leu Ile Phe Ala Ile Met Gly Val Gln Leu Phe Ala Gly Lys
    1410              1415              1420

Tyr Phe Lys Cys Glu Asp Met Asn Gly Thr Lys Leu Ser His Glu Ile
1425              1430              1435              1440

Ile Pro Asn Arg Asn Ala Cys Glu Ser Glu Asn Tyr Thr Trp Val Asn
              1445              1450              1455

Ser Ala Met Asn Phe Asp His Val Gly Asn Ala Tyr Leu Cys Leu Phe
              1460              1465              1470

Gln Val Ala Thr Phe Lys Gly Trp Ile Gln Ile Met Asn Asp Ala Ile
    1475              1480              1485

Asp Ser Arg Glu Val Asp Lys Gln Pro Ile Arg Glu Thr Asn Ile Tyr
    1490              1495              1500
```

Met Tyr Leu Tyr Phe Val Phe Phe Ile Ile Phe Gly Ser Phe Phe Thr
1505                1510                1515                1520

Leu Asn Leu Phe Ile Gly Val Ile Ile Asp Asn Phe Asn Glu Gln Lys
                1525                1530                1535

Lys Lys Ala Gly Gly Ser Leu Glu Met Phe Met Thr Glu Asp Gln Lys
                1540                1545                1550

Lys Tyr Tyr Ser Ala Met Lys Lys Met Gly Ser Lys Lys Pro Leu Lys
                1555                1560                1565

Ala Ile Pro Arg Pro Arg Trp Arg Pro Gln Ala Ile Val Phe Glu Ile
                1570                1575                1580

Val Thr Asp Lys Lys Phe Asp Ile Ile Ile Met Leu Phe Ile Gly Leu
1585                1590                1595                1600

Asn Met Phe Thr Met Thr Leu Asp Arg Tyr Asp Ala Ser Asp Thr Tyr
                1605                1610                1615

Asn Ala Val Leu Asp Tyr Leu Asn Ala Ile Phe Val Val Ile Phe Ser
                1620                1625                1630

Ser Glu Cys Leu Leu Lys Ile Phe Ala Leu Arg Tyr His Tyr Phe Ile
                1635                1640                1645

Glu Pro Trp Asn Leu Phe Asp Val Val Val Val Ile Leu Ser Ile Leu
                1650                1655                1660

Gly Leu Val Leu Ser Asp Ile Ile Glu Lys Tyr Phe Val Ser Pro Thr
1665                1670                1675                1680

Leu Leu Arg Val Val Arg Val Ala Lys Val Gly Arg Val Leu Arg Leu
                1685                1690                1695

Val Lys Gly Ala Lys Gly Ile Arg Thr Leu Leu Phe Ala Leu Ala Met
                1700                1705                1710

Ser Leu Pro Ala Leu Phe Asn Ile Cys Leu Leu Leu Phe Leu Val Met
                1715                1720                1725

Phe Ile Phe Ala Ile Phe Gly Met Ser Phe Phe Met His Val Lys Glu
                1730                1735                1740

Lys Ser Gly Ile Asn Asp Val Tyr Asn Phe Lys Thr Phe Gly Gln Ser
1745                1750                1755                1760

Met Ile Leu Leu Phe Gln Met Ser Thr Ser Ala Gly Trp Asp Gly Val
　　　　　　　　　1765　　　　　　　1770　　　　　　1775

Leu Asp Ala Ile Ile Asn Glu Glu Ala Cys Asp Pro Pro Asp Asn Asp
　　　　　　　　1780　　　　　　1785　　　　　　1790

Lys Gly Tyr Pro Gly Asn Cys Gly Ser Ala Thr Val Gly Ile Thr Phe
　　　　　1795　　　　　　　1800　　　　　1805

Leu Leu Ser Tyr Leu Val Ile Ser Phe Leu Ile Val Ile Asn Met Tyr .
　　1810　　　　　　1815　　　　　　1820

Ile Ala Val Ile Leu Glu Asn Tyr Ser Gln Ala Thr Glu Asp Val Gln
1825　　　　　　1830　　　　　　1835　　　　　　　1840

Glu Gly Leu Thr Asp Asp Asp Tyr Asp Met Tyr Tyr Glu Ile Trp Gln
　　　　　　　1845　　　　　　1850　　　　　1855

Gln Phe Asp Pro Glu Gly Thr Gln Tyr Ile Arg Tyr Asp Gln Leu Ser
　　　　　1860　　　　　　1865　　　　　1870

Glu Phe Leu Asp Val Leu Glu Pro Pro Leu Gln Ile His Lys Pro Asn
　　　1875　　　　　　1880　　　　　1885

Lys Tyr Lys Ile Ile Ser Met Asp Ile Pro Ile Cys Arg Gly Asp Leu
　　1890　　　　　1895　　　　　1900

Met Tyr Cys Val Asp Ile Leu Asp Ala Leu Thr Lys Asp Phe Phe Ala
1905　　　　　1910　　　　　1915　　　　　1920

Arg Lys Gly Asn Pro Ile Glu Glu Thr Gly Glu Ile Gly Glu Ile Ala
　　　　　1925　　　　　　1930　　　　　1935

Ala Arg Pro Asp Thr Glu Gly Tyr Glu Pro Val Ser Ser Thr Leu Trp
　　　1940　　　　　　1945　　　　　1950

Arg Gln Arg Glu Glu Tyr Cys Ala Arg Leu Ile Gln His Ala Trp Arg
　　　1955　　　　　1960　　　　　1965

Lys His Lys Ala Arg Gly Glu Gly Gly Gly Ser Phe Glu Pro Asp Thr
　　1970　　　　　1975　　　　　1980

Asp His Gly Asp Gly Gly Asp Pro Asp Ala Gly Asp Pro Ala Pro Asp
1985　　　　　1990　　　　　1995　　　　　2000

Glu Ala Thr Asp Gly Asp Ala Pro Ala Gly Gly Asp Gly Ser Val Asn
　　　　　2005　　　　　2010　　　　　2015

Gly Thr Ala Glu Gly Ala Ala Asp Ala Asp Glu Ser Asn Val Asn Ser
        2020                  2025             2030

Pro Gly Glu Asp Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala
        2035            2040             2045

Ala Ala Gly Thr Thr Thr Ala Gly Ser Pro Gly Ala Gly Ser Ala Gly
        2050           2055            2060

Arg Gln Thr Ala Val Leu Val Glu Ser Asp Gly Phe Val Thr Lys Asn
2065             2070          2075           2080

Gly His Lys Val Val Ile His Ser Arg Ser Pro Ser Ile Thr Ser Arg
        2085           2090           2095

Thr Ala Asp Val
        2100